

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Brown, John, Kinney, Anthony J.,
Pierce, John, Wierzbicki, Anna M.,
Yadav, Narendra S., Perez-Grau, Luis
- (ii) TITLE OF INVENTION: Fatty Acid Desaturase Genes
from Plants
- (iii) NUMBER OF SEQUENCES: 32
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: E. I. du Pont de Nemours and Company
(B) STREET: 1007 Market Street
(C) CITY: Wilmington
(D) STATE: Delaware
(E) COUNTRY: U.S.A.
(F) ZIP: 19898
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Macintosh
(C) OPERATING SYSTEM: Macintosh System, 6.0
(D) SOFTWARE: Microsoft Word, 4.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/804,259
(B) FILING DATE: 4 DECEMBER 1991
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Floyd, Linda A.
(B) REGISTRATION NUMBER: 33,692
(C) REFERENCE/DOCKET NUMBER: BB-1036-A
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (302) 992-4929
(B) TELEFAX: (302) 892-7949
(C) TELEX: 835420

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana* IMMEDIATE SOURCE:
 (B) CLONE: pCF3

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 46..1206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCTCTCTCT CTCTCTTCTC TCTTTCTCTC CCCCTCTCTC CGGCG ATG GTT GTT	54
Met Val Val	
1	
GCT ATG GAC CAA CGC ACC AAT GTG AAC GGA GAT CCC GGC GCC GGA GAC	102
Ala Met Asp Gln Arg Thr Asn Val Asn Gly Asp Pro Gly Ala Gly Asp	
5 10 15	
CGG AAG AAA GAA GAA AGG TTT GAT CCG AGT GCA CAA CCA CCG TTC AAG	150
Arg Lys Lys Glu Glu Arg Phe Asp Pro Ser Ala Gln Pro Pro Phe Lys	
20 25 30 35	
ATC GGA GAT ATA AGG GCG GCG ATT CCT AAG CAC TGT TGG GTT AAG AGT	198
Ile Gly Asp Ile Arg Ala Ala Ile Pro Lys His Cys Trp Val Lys Ser	
40 45 50	
CCT TTG AGA TCA ATG AGT TAC GTC GTC AGA GAC ATT ATC GCC GTC GCG	246
Pro Leu Arg Ser Met Ser Tyr Val Val Arg Asp Ile Ile Ala Val Ala	
55 60 65	
GCT TTG GCC ATC GCT GCC GTG TAT GTT GAT AGC TGG TTC CTT TGG CCT	294
Ala Leu Ala Ile Ala Ala Val Tyr Val Asp Ser Trp Phe Leu Trp Pro	
70 75 80	
CTT TAT TGG GCC GCC CAA GGA ACA CTT TTC TGG GCC ATC TTT GTT CTC	342
Leu Tyr Trp Ala Ala Gln Gly Thr Leu Phe Trp Ala Ile Phe Val Leu	
85 90 95	
GGC CAC GAC TGT GGA CAT GGG AGT TTC TCA GAC ATT CCT CTA CTG AAT	390
Gly His Asp Cys Gly His Gly Ser Phe Ser Asp Ile Pro Leu Leu Asn	
100 105 110 115	

BBE22T 32561250

AGT Ser	GTG Val	GTT Val	GGT Gly	CAC His 120	ATT Ile	CTT Leu	CAT His	TCT Ser	TTC Phe 125	ATC Ile	CTC Leu	GTT Val	CCT Pro	TAC Tyr 130	CAT His	438
GGT Gly	TGG Trp	AGA Arg	ATA Ile 135	AGC Ser	CAC His	CGG Arg	ACA Thr	CAC His 140	CAC His	CAG Gln	AAC Asn	CAT His	GGC Gly 145	CAT His	GTT Val	486
GAA Glu	AAC Asn	GAC Asp 150	GAG Glu	TCA Ser	TGG Trp	GTT Val	CCG Pro 155	TTA Leu	CCA Pro	GAA Glu	AGG Arg	GTG Val 160	TAC Tyr	AAG Lys	AAA Lys	534
TTG Leu	CCC Pro 165	CAC His	AGT Ser	ACT Thr	CGG Arg	ATG Met 170	CTC Leu	AGA Arg	TAC Tyr	ACT Thr	GTC Val 175	CCT Pro	CTC Leu	CCC Pro	ATG Met	582
CTC Leu 180	GCA Ala	TAT Tyr	CCT Pro	CTC Leu	TAT Tyr 185	TTG Leu	TGC Cys	TAC Tyr	AGA Arg	AGT Ser 190	CCT Pro	GGA Gly	AAA Lys	GAA Glu	GGA Gly 195	630
TCA Ser	CAT His	TTT Phe	AAC Asn 200	CCA Pro	TAC Tyr	AGT Ser	AGT Ser	TTA Leu 205	TTT Phe	GCT Ala	CCA Pro	AGC Ser	GAG Glu	AGA Arg 210	AAG Lys	678
CTT Leu	ATT Ile	GCA Ala	ACT Thr 215	TCA Ser	ACT Thr	ACT Thr	TGT Cys	TGG Trp 220	TCC Ser	ATA Ile	ATG Met	TTC Phe	GTC Val 225	AGT Ser	CTT Leu	726
ATC Ile	GCT Ala	CTA Leu 230	TCT Ser	TTC Phe	GTC Val	TTC Phe	GGT Gly 235	CCA Pro	CTC Leu	GCG Ala	GTT Val	CTT Leu 240	AAA Lys	GTC Val	TAC Tyr	774
GGT Gly	GTA Val 245	CCG Pro	TAC Tyr	ATT Ile	ATC Ile	TTT Phe 250	GTG Val	ATG Met	TGG Trp	TTG Leu	GAT Asp 255	GCT Ala	GTC Val	ACG Thr	TAT Tyr	822
TTG Leu 260	CAT His	CAT His	CAT His	GGT Gly	CAC His 265	GAT Asp	GAG Glu	AAG Lys	TTG Leu	CCT Pro 270	TGG Trp	TAT Tyr	AGA Arg	GGC Gly	AAG Lys 275	870
GAA Glu	TGG Trp	AGT Ser	TAT Tyr 280	CTA Leu	CGT Arg	GGA Gly	GGA Gly	TTA Leu 285	ACA Thr	ACA Thr	ATT Ile	GAT Asp	AGA Arg	GAT Asp 290	TAC Tyr	918
GGA Gly	ATC Ile	TTT Phe	AAC Asn 295	AAC Asn	ATT Ile	CAT His	CAC His	GAC Asp 300	ATT Ile	GGA Gly	ACT Thr	CAC His	GTG Val 305	ATC Ile	CAT His	966
CAT His	CTC Leu	TTC Phe 310	CCA Pro	CAA Gln	ATC Ile	CCT Pro	CAC His 315	TAT Tyr	CAC His	TTG Leu	GTC Val	GAC Asp 320	GCC Ala	ACG Thr	AAA Lys	1014
GCA Ala	GCT Ala	AAA Lys 325	CAT His	GTG Val	TTG Leu	GGA Gly 330	AGA Arg	TAC Tyr	TAC Tyr	AGA Arg	GAA Glu 335	CCA Pro	AAG Lys	ACG Thr	TCA Ser	1062

(2) INFORMATION FOR SEQ. ID NO:2:

(A) LENGTH: 386 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Val	Ala	Met	Asp	Gln	Arg	Thr	Asn	Val	Asn	Gly	Asp	Pro	Gly
1				5					10					15	
Ala	Gly	Asp	Arg	Lys	Lys	Glu	Glu	Arg	Phe	Asp	Pro	Ser	Ala	Gln	Pro
			20					25					30		
Pro	Phe	Lys	Ile	Gly	Asp	Ile	Arg	Ala	Ala	Ile	Pro	Lys	His	Cys	Trp
		35					40					45			
Val	Lys	Ser	Pro	Leu	Arg	Ser	Met	Ser	Tyr	Val	Val	Arg	Asp	Ile	Ile
	50					55					60				
Ala	Val	Ala	Ala	Leu	Ala	Ile	Ala	Ala	Val	Tyr	Val	Asp	Ser	Trp	Phe
65					70					75					80
Leu	Trp	Pro	Leu	Tyr	Trp	Ala	Ala	Gln	Gly	Thr	Leu	Phe	Trp	Ala	Ile
				85					90					95	
Phe	Val	Leu	Gly	His	Asp	Cys	Gly	His	Gly	Ser	Phe	Ser	Asp	Ile	Pro
			100					105					110		
Leu	Leu	Asn	Ser	Val	Val	Gly	His	Ile	Leu	His	Ser	Phe	Ile	Leu	Val
		115					120					125			
Pro	Tyr	His	Gly	Trp	Arg	Ile	Ser	His	Arg	Thr	His	His	Gln	Asn	His
	130					135					140				

Gly His Val Glu Asn Asp Glu Ser Trp Val Pro Leu Pro Glu Arg Val
 145 150 155 160
 Tyr Lys Lys Leu Pro His Ser Thr Arg Met Leu Arg Tyr Thr Val Pro
 165 170 175
 Leu Pro Met Leu Ala Tyr Pro Leu Tyr Leu Cys Tyr Arg Ser Pro Gly
 180 185 190
 Lys Glu Gly Ser His Phe Asn Pro Tyr Ser Ser Leu Phe Ala Pro Ser
 195 200 205
 Glu Arg Lys Leu Ile Ala Thr Ser Thr Thr Cys Trp Ser Ile Met Phe
 210 215 220
 Val Ser Leu Ile Ala Leu Ser Phe Val Phe Gly Pro Leu Ala Val Leu
 225 230 235 240
 Lys Val Tyr Gly Val Pro Tyr Ile Ile Phe Val Met Trp Leu Asp Ala
 245 250 255
 Val Thr Tyr Leu His His His Gly His Asp Glu Lys Leu Pro Trp Tyr
 260 265 270
 Arg Gly Lys Glu Trp Ser Tyr Leu Arg Gly Gly Leu Thr Thr Ile Asp
 275 280 285
 Arg Asp Tyr Gly Ile Phe Asn Asn Ile His His Asp Ile Gly Thr His
 290 295 300
 Val Ile His His Leu Phe Pro Gln Ile Pro His Tyr His Leu Val Asp
 305 310 315 320
 Ala Thr Lys Ala Ala Lys His Val Leu Gly Arg Tyr Tyr Arg Glu Pro
 325 330 335
 Lys Thr Ser Gly Ala Ile Pro Ile His Leu Val Glu Ser Leu Val Ala
 340 345 350
 Ser Ile Lys Lys Asp His Tyr Val Ser Asp Thr Gly Asp Ile Val Phe
 355 360 365
 Tyr Glu Thr Asp Pro Asp Leu Tyr Val Tyr Ala Ser Asp Lys Ser Lys
 370 375 380
 Ile Asn
 385

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AAATTCATCA	AACCCCTTCT	TCACCACATT	ATTTTCACTG	AGCGCATAAC	ATTTTTGAGA	60
CAAGAGACTC	TCTCTCTCTC	TCTTCTCTCT	TTCTCTCCCC	CTCTCTCCGG	CGATGGTTGT	120
TGCTATGGAC	CAACGCACCA	ATGTGAACGG	AGATCCCGGC	GCCGGAGACC	GGAAGAAAGA	180
AGAAAGGTTT	GATCCGAGTG	CACAACCACC	GTTCAAGATC	GGAGATATAA	GGGCGGCGAT	240
TCCTAAGCAC	TGTTG					255

(i) SEQUENCE CHARACTERISTICS:

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

      (A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

      (B) CLONE: pACF2-2

(ix) FEATURE:

      (A) NAME/KEY: CDS
      (B) LOCATION: 10..1350

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAAGTTCTA ATG GCG AAC TTG GTC TTA TCA GAA TGT GGT ATA CGA CCT	48
Met Ala Asn Leu Val Leu Ser Glu Cys Gly Ile Arg Pro	
1 5 10	
CTC CCC AGA ATC TAC ACA ACA CCC AGA TCC AAT TTC CTC TCC AAC AAC	96
Leu Pro Arg Ile Tyr Thr Thr Pro Arg Ser Asn Phe Leu Ser Asn Asn	
15 20 25	
AAC AAA TTC AGA CCA TCA CTT TCT TCT TCT TCT TAC AAA ACA TCA TCA	144
Asn Lys Phe Arg Pro Ser Leu Ser Ser Ser Tyr Lys Thr Ser Ser	
30 35 40 45	
TCT CCT CTG TCT TTT GGT CTG AAT TCA CGA GAT GGG TTC ACG AGG AAT	192
Ser Pro Leu Ser Phe Gly Leu Asn Ser Arg Asp Gly Phe Thr Arg Asn	
50 55 60	
TGG GCG TTG AAT GTG AGC ACA CCA TTA ACG ACA CCA ATA TTT GAG GAG	240
Trp Ala Leu Asn Val Ser Thr Pro Leu Thr Thr Pro Ile Phe Glu Glu	
65 70 75	
TCT CCA TTG GAG GAA GAT AAT AAA CAG AGA TTC GAT CCA GGT GCG CCT	288
Ser Pro Leu Glu Glu Asp Asn Lys Gln Arg Phe Asp Pro Gly Ala Pro	
80 85 90	
CCT CCG TTC AAT TTA GCT GAT ATT AGA GCA GCT ATA CCT AAG CAT TGT	336
Pro Pro Phe Asn Leu Ala Asp Ile Arg Ala Ala Ile Pro Lys His Cys	
95 100 105	
TGG GTT AAG AAT CCA TGG AAG TCT TTG AGT TAT GTC GTC AGA GAC GTC	384
Trp Val Lys Asn Pro Trp Lys Ser Leu Ser Tyr Val Val Arg Asp Val	
110 115 120 125	
GCT ATC GTC TTT GCA TTG GCT GCT GGA GCT GCT TAC CTC AAC AAT TGG	432
Ala Ile Val Phe Ala Leu Ala Ala Gly Ala Ala Tyr Leu Asn Asn Trp	
130 135 140	
ATT GTT TGG CCT CTC TAT TGG CTC GCT CAA GGA ACC ATG TTT TGG GCT	480
Ile Val Trp Pro Leu Tyr Trp Leu Ala Gln Gly Thr Met Phe Trp Ala	
145 150 155	
CTC TTT GTT CTT GGT CAT GAC TGT GGA CAT GGT AGT TTC TCA AAT GAT	528
Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser Asn Asp	
160 165 170	
CCG AAG TTG AAC AGT GTG GTC GGT CAT CTT CTT CAT TCC TCA ATT CTG	576
Pro Lys Leu Asn Ser Val Val Gly His Leu Leu His Ser Ser Ile Leu	
175 180 185	
GTC CCA TAC CAT GGC TGG AGA ATT AGT CAC AGA ACT CAC CAC CAG AAC	624
Val Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn	
190 195 200 205	
CAT GGA CAT GTT GAG AAT GAC GAA TCT TGG CAT CCT ATG TCT GAG AAA	672
His Gly His Val Glu Asn Asp Glu Ser Trp His Pro Met Ser Glu Lys	
210 215 220	

BBEET 00000000

[illegible]

ATTTTTTGCT TACTGTATCA ATTTATTGTG TCACCCACCA GAGAGTTAGT ATCTCTGAAT 1457
 ACGATCGATC AGATGGAAAC AACAAATTTG TTTGCGATAC TGAAGCTATA TATACCATAC 1517
 ATTGCATT 1525

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Asn Leu Val Leu Ser Glu Cys Gly Ile Arg Pro Leu Pro Arg
 1 5 10 15
 Ile Tyr Thr Thr Pro Arg Ser Asn Phe Leu Ser Asn Asn Asn Lys Phe
 20 25 30
 Arg Pro Ser Leu Ser Ser Ser Ser Tyr Lys Thr Ser Ser Ser Pro Leu
 35 40 45
 Ser Phe Gly Leu Asn Ser Arg Asp Gly Phe Thr Arg Asn Trp Ala Leu
 50 55 60
 Asn Val Ser Thr Pro Leu Thr Thr Pro Ile Phe Glu Glu Ser Pro Leu
 65 70 75 80
 Glu Glu Asp Asn Lys Gln Arg Phe Asp Pro Gly Ala Pro Pro Pro Phe
 85 90 95
 Asn Leu Ala Asp Ile Arg Ala Ala Ile Pro Lys His Cys Trp Val Lys
 100 105 110
 Asn Pro Trp Lys Ser Leu Ser Tyr Val Val Arg Asp Val Ala Ile Val
 115 120 125
 Phe Ala Leu Ala Ala Gly Ala Ala Tyr Leu Asn Asn Trp Ile Val Trp
 130 135 140
 Pro Leu Tyr Trp Leu Ala Gln Gly Thr Met Phe Trp Ala Leu Phe Val
 145 150 155 160
 Leu Gly His Asp Cys Gly His Gly Ser Phe Ser Asn Asp Pro Lys Leu
 165 170 175
 Asn Ser Val Val Gly His Leu Leu His Ser Ser Ile Leu Val Pro Tyr
 180 185 190
 His Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn His Gly His
 195 200 205

052227 32667260

Val Glu Asn Asp Glu Ser Trp His Pro Met Ser Glu Lys Ile Tyr Asn
 210 215 220
 Thr Leu Asp Lys Pro Thr Arg Phe Phe Arg Phe Thr Leu Pro Leu Val
 225 230 235 240
 Met Leu Ala Tyr Pro Phe Tyr Leu Trp Ala Arg Ser Pro Gly Lys Lys
 245 250 255
 Gly Ser His Tyr His Pro Asp Ser Asp Leu Phe Leu Pro Lys Glu Arg
 260 265 270
 Lys Asp Val Leu Thr Ser Thr Ala Cys Trp Thr Ala Met Ala Ala Leu
 275 280 285
 Leu Val Cys Leu Asn Phe Thr Ile Gly Pro Ile Gln Met Leu Lys Leu
 290 295 300
 Tyr Gly Ile Pro Tyr Trp Ile Asn Val Met Trp Leu Asp Phe Val Thr
 305 310 315 320
 Tyr Leu His His His Gly His Glu Asp Lys Leu Pro Trp Tyr Arg Gly
 325 330 335
 Lys Glu Trp Ser Tyr Leu Arg Gly Gly Leu Thr Thr Leu Asp Arg Asp
 340 345 350
 Tyr Gly Leu Ile Asn Asn Ile His His Asp Ile Gly Thr His Val Ile
 355 360 365
 His His Leu Phe Pro Gln Ile Pro His Tyr His Leu Val Glu Ala Thr
 370 375 380
 Glu Ala Ala Lys Pro Val Leu Gly Lys Tyr Tyr Arg Glu Pro Asp Lys
 385 390 395 400
 Ser Gly Pro Leu Pro Leu His Leu Leu Glu Ile Leu Ala Lys Ser Ile
 405 410 415
 Lys Glu Asp His Tyr Val Ser Asp Glu Gly Glu Val Val Tyr Tyr Lys
 420 425 430
 Ala Asp Pro Asn Leu Tyr Gly Glu Val Lys Val Arg Ala Asp
 435 440 445

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

0921993E 122996

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Brassica napus

(vii) IMMEDIATE SOURCE:

(B) CLONE: pBNSF3-f2

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 79..1212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCAAATTCA GACAATCCCC TTCTTCTCCC CGGTTTCGTC TGAACTCTCG AAACCTGGGCG	60
TTGAATGTAA CCACACCT CTA ACA GTC GAC TCC TCA TCA TCT CCT CCA ATC	111
Leu Thr Val Asp Ser Ser Ser Ser Pro Pro Ile	
1 5 10	
GAG GAA GAA CCC AAA ACG CAG AGA TTC GAC CCA GGC GCT CCT CCT CCG	159
Glu Glu Glu Pro Lys Thr Gln Arg Phe Asp Pro Gly Ala Pro Pro Pro	
15 20 25	
TTC AAC CTA GCT GAC ATC AGA GCG GCG ATA CCT AAG CAT TGC TGG GTT	207
Phe Asn Leu Ala Asp Ile Arg Ala Ala Ile Pro Lys His Cys Trp Val	
30 35 40	
AAG AAT CCA TGG AAG TCT ATG AGT TAC GTC GTC AGA GAG CTA GCC ATC	255
Lys Asn Pro Trp Lys Ser Met Ser Tyr Val Val Arg Glu Leu Ala Ile	
45 50 55	
GTG TTC GCA CTA GCT GCT GGA GCT GCT TAC CTC AAC AAT TGG CTT GTT	303
Val Phe Ala Leu Ala Ala Gly Ala Ala Tyr Leu Asn Asn Trp Leu Val	
60 65 70 75	
TGG CCT CTC TAT TGG ATT GCT CAA GGA ACC ATG TTC TGG GCT CTC TTT	351
Trp Pro Leu Tyr Trp Ile Ala Gln Gly Thr Met Phe Trp Ala Leu Phe	
80 85 90	
GTT CTT GGC CAT GAC TGT GGA CAT GGA AGC TTC TCA AAT GAT CCG AGG	399
Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser Asn Asp Pro Arg	
95 100 105	
TTG AAC AGT GTG GTG GGT CAC CTT CTT CAT TCC TCT ATT CTA GTC CCT	447
Leu Asn Ser Val Val Gly His Leu Leu His Ser Ser Ile Leu Val Pro	
110 115 120	
TAC CAT GGC TGG AGA ATT AGC CAC AGA ACT CAC CAC CAG AAC CAT GGA	495
Tyr His Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn His Gly	
125 130 135	
CAT GTT GAG AAC GAT GAA TCT TGG CAT CCT ATG TCT GAG AAA ATC TAC	543
His Val Glu Asn Asp Glu Ser Trp His Pro Met Ser Glu Lys Ile Tyr	
140 145 150 155	

SECRET

AAG AGT TTG GAC AAA CCC ACT CGG TTC TTT AGA TTT ACA TTG CCT CTC	591
Lys Ser Leu Asp Lys Pro Thr Arg Phe Phe Arg Phe Thr Leu Pro Leu	
160 165 170	
GTG ATG CTC GCT TAC CCT TTC TAC TTG TGG GCA AGA AGT CCA GGG AAG	639
Val Met Leu Ala Tyr Pro Phe Tyr Leu Trp Ala Arg Ser Pro Gly Lys	
175 180 185	
AAG GGT TCT CAT TAC CAT CCA GAC AGC GAC TTG TTC CTT CCT AAA GAG	687
Lys Gly Ser His Tyr His Pro Asp Ser Asp Leu Phe Leu Pro Lys Glu	
190 195 200	
AGA AAC GAT GTT CTC ACT TCT ACC GCT TGT TGG ACT GCA ATG GCT GTT	735
Arg Asn Asp Val Leu Thr Ser Thr Ala Cys Trp Thr Ala Met Ala Val	
205 210 215	
CTG CTT GTC TGT CTC AAC TTC GTG ATG GGT CCA ATG CAA ATG CTC AAA	783
Leu Leu Val Cys Leu Asn Phe Val Met Gly Pro Met Gln Met Leu Lys	
220 225 230 235	
CTT TAT GTC ATT CCT TAC TGG ATA AAT GTA ATG TGG TTG GAC TTT GTG	831
Leu Tyr Val Ile Pro Tyr Trp Ile Asn Val Met Trp Leu Asp Phe Val	
240 245 250	
ACT TAC CTG CAT CAC CAT GGT CAT GAA GAT AAG CTC CCT TGG TAC CGT	879
Thr Tyr Leu His His His Gly His Glu Asp Lys Leu Pro Trp Tyr Arg	
255 260 265	
GGG AAG GAA TGG AGT TAC TTG AGA GGA GGA CTT ACA ACA TTG GAC CGG	927
Gly Lys Glu Trp Ser Tyr Leu Arg Gly Gly Leu Thr Thr Leu Asp Arg	
270 275 280	
GAC TAC GGA TTG ATC AAC AAC ATC CAT CAC GAC ATT GGA ACT CAT GTG	975
Asp Tyr Gly Leu Ile Asn Asn Ile His His Asp Ile Gly Thr His Val	
285 290 295	
ATA CAT CAT CTT TTC CCT CAG ATC CCA CAT TAT CAT CTA GTA GAA GCA	1023
Ile His His Leu Phe Pro Gln Ile Pro His Tyr His Leu Val Glu Ala	
300 305 310 315	
ACA GAA GCA GCT AAA CCA GTA TTA GGG AAG TAT TAT AGG GAG CCT GAT	1071
Thr Glu Ala Ala Lys Pro Val Leu Gly Lys Tyr Tyr Arg Glu Pro Asp	
320 325 330	
AAG TCT GGA CCT TTG CCA TTA CAT TTA CTG GGA ATC TTA GCA AAA AGT	1119
Lys Ser Gly Pro Leu Pro Leu His Leu Leu Gly Ile Leu Ala Lys Ser	
335 340 345	
ATT AAA GAA GAT CAT TTT GTG AGC GAT GAA GGA GAT GTT GTA TAC TAT	1167
Ile Lys Glu Asp His Phe Val Ser Asp Glu Gly Asp Val Val Tyr Tyr	
350 355 360	
GAA GCA GAC CCT AAT CTC TAT GGA GAG ATC AAG GTA ACA GCA GAG	1212
Glu Ala Asp Pro Asn Leu Tyr Gly Glu Ile Lys Val Thr Ala Glu	
365 370 375	
TGAAATGAAG CTGTCAGATT TATCTATTTT TGACCAGCTG ATTTTTTTTG CTTATTAATG	1272

(2) INFORMATION FOR SEO ID NO:7:

(A) LENGTH: 378 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:7:

Leu 1	Thr	Val	Asp	Ser 5	Ser	Ser	Ser	Pro 10	Ile	Glu	Glu	Glu	Pro 15	Lys	
Thr	Gln	Arg	Phe 20	Asp	Pro	Gly	Ala	Pro 25	Pro	Pro	Phe	Asn	Leu 30	Ala	Asp
Ile	Arg	Ala 35	Ala	Ile	Pro	Lys	His 40	Cys	Trp	Val	Lys	Asn 45	Pro	Trp	Lys
Ser	Met 50	Ser	Tyr	Val	Val	Arg 55	Glu	Leu	Ala	Ile	Val 60	Phe	Ala	Leu	Ala
Ala 65	Gly	Ala	Ala	Tyr	Leu 70	Asn	Asn	Trp	Leu	Val 75	Trp	Pro	Leu	Tyr	Trp 80
Ile	Ala	Gln	Gly	Thr 85	Met	Phe	Trp	Ala	Leu 90	Phe	Val	Leu	Gly	His 95	Asp
Cys	Gly	His	Gly 100	Ser	Phe	Ser	Asn	Asp 105	Pro	Arg	Leu	Asn	Ser 110	Val	Val
Gly	His 115	Leu	Leu	His	Ser	Ser	Ile 120	Leu	Val	Pro	Tyr	His 125	Gly	Trp	Arg
Ile 130	Ser	His	Arg	Thr	His	His 135	Gln	Asn	His	Gly	His 140	Val	Glu	Asn	Asp
Glu 145	Ser	Trp	His	Pro	Met 150	Ser	Glu	Lys	Ile	Tyr 155	Lys	Ser	Leu	Asp	Lys 160
Pro	Thr	Arg	Phe	Phe 165	Arg	Phe	Thr	Leu	Pro 170	Leu	Val	Met	Leu	Ala 175	Tyr
Pro	Phe	Tyr	Leu 180	Trp	Ala	Arg	Ser	Pro 185	Gly	Lys	Lys	Gly	Ser 190	His	Tyr
His	Pro 195	Asp	Ser	Asp	Leu	Phe	Leu 200	Pro	Lys	Glu	Arg	Asn 205	Asp	Val	Leu

Thr Ser Thr Ala Cys Trp Thr Ala Met Ala Val Leu Leu Val Cys Leu
 210 215 220
 Asn Phe Val Met Gly Pro Met Gln Met Leu Lys Leu Tyr Val Ile Pro
 225 230 235 240
 Tyr Trp Ile Asn Val Met Trp Leu Asp Phe Val Thr Tyr Leu His His
 245 250 255
 His Gly His Glu Asp Lys Leu Pro Trp Tyr Arg Gly Lys Glu Trp Ser
 260 265 270
 Tyr Leu Arg Gly Gly Leu Thr Thr Leu Asp Arg Asp Tyr Gly Leu Ile
 275 280 285
 Asn Asn Ile His His Asp Ile Gly Thr His Val Ile His His Leu Phe
 290 295 300
 Pro Gln Ile Pro His Tyr His Leu Val Glu Ala Thr Glu Ala Ala Lys
 305 310 315 320
 Pro Val Leu Gly Lys Tyr Tyr Arg Glu Pro Asp Lys Ser Gly Pro Leu
 325 330 335
 Pro Leu His Leu Leu Gly Ile Leu Ala Lys Ser Ile Lys Glu Asp His
 340 345 350
 Phe Val Ser Asp Glu Gly Asp Val Val Tyr Tyr Glu Ala Asp Pro Asn
 355 360 365
 Leu Tyr Gly Glu Ile Lys Val Thr Ala Glu
 370 375

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Brassica napus

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pBNSFd-2

0921935 132345
 0921935 132345

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..1215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTC AAA TTC AGA CAA TCC CCT TCT TCT CCC CGG TTT CGT CTG AAC TCT	48
Phe Lys Phe Arg Gln Ser Pro Ser Ser Pro Arg Phe Arg Leu Asn Ser	
1 5 10 15	
CGA AAC TGG GCG TTG AAT GTA ACC ACA CCT CTA ACA GTC GAC TCC TCA	96
Arg Asn Trp Ala Leu Asn Val Thr Thr Pro Leu Thr Val Asp Ser Ser	
20 25 30	
TCA TCT CCT CCA ATC GAG GAA GAA CCC AAA ACG CAG AGA TTC GAC CCA	144
Ser Ser Pro Pro Ile Glu Glu Glu Pro Lys Thr Gln Arg Phe Asp Pro	
35 40 45	
GGC GCT CCT CCT CCG TTC AAC CTA GCT GAC ATC AGA GCG GCG ATA CCT	192
Gly Ala Pro Pro Pro Phe Asn Leu Ala Asp Ile Arg Ala Ala Ile Pro	
50 55 60	
AAG CAT TGC TGG GTT AAG AAT CCA TGG AAG TCT ATG AGT TAC GTC GTC	240
Lys His Cys Trp Val Lys Asn Pro Trp Lys Ser Met Ser Tyr Val Val	
65 70 75 80	
AGA GAG CTA GCC ATC GTG TTC GCA CTA GCT GCT GGA GCT GCT TAC CTC	288
Arg Glu Leu Ala Ile Val Phe Ala Leu Ala Ala Gly Ala Ala Tyr Leu	
85 90 95	
AAC AAT TGG CTT GTT TGG CCT CTC TAT TGG ATT GCT CAA GGA ACC ATG	336
Asn Asn Trp Leu Val Trp Pro Leu Tyr Trp Ile Ala Gln Gly Thr Met	
100 105 110	
TTC TGG GCT CTC TTT GTT CTT GGC CAT GAC TGT GGA CAT GGA AGC TTC	384
Phe Trp Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe	
115 120 125	
TCA AAT GAT CCG AGG TTG AAC AGT GTG GTG GGT CAC CTT CTT CAT TCC	432
Ser Asn Asp Pro Arg Leu Asn Ser Val Val Gly His Leu Leu His Ser	
130 135 140	
TCT ATT CTA GTC CCT TAC CAT GGC TGG AGA ATT AGC CAC AGA ACT CAC	480
Ser Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His	
145 150 155 160	
CAC CAG AAC CAT GGA CAT GTT GAG AAC GAT GAA TCT TGG CAT CCT ATG	528
His Gln Asn His Gly His Val Glu Asn Asp Glu Ser Trp His Pro Met	
165 170 175	
TCT GAG AAA ATC TAC AAG AGT TTG GAC AAA CCC ACT CGG TTC TTT AGA	576
Ser Glu Lys Ile Tyr Lys Ser Leu Asp Lys Pro Thr Arg Phe Phe Arg	
180 185 190	
TTT ACA TTG CCT CTC GTG ATG CTC GCT TAC CCT TTC TAC TTG TGG GCA	624
Phe Thr Leu Pro Leu Val Met Leu Ala Tyr Pro Phe Tyr Leu Trp Ala	
195 200 205	

0001995 12290

AGA AGT CCA GGG AAG AAG GGT TCT CAT TAC CAT CCA GAC AGC GAC TTG	672
Arg Ser Pro Gly Lys Lys Gly Ser His Tyr His Pro Asp Ser Asp Leu	
210 215 220	
TTC CTT CCT AAA GAG AGA AAC GAT GTT CTC ACT TCT ACC GCT TGT TGG	720
Phe Leu Pro Lys Glu Arg Asn Asp Val Leu Thr Ser Thr Ala Cys Trp	
225 230 235 240	
ACT GCA ATG GCT GTT CTG CTT GTC TGT CTC AAC TTC GTG ATG GGT CCA	768
Thr Ala Met Ala Val Leu Leu Val Cys Leu Asn Phe Val Met Gly Pro	
245 250 255	
ATG CAA ATG CTC AAA CTT TAT GTC ATT CCT TAC TGG ATA AAT GTA ATG	816
Met Gln Met Leu Lys Leu Tyr Val Ile Pro Tyr Trp Ile Asn Val Met	
260 265 270	
TGG TTG GAC TTT GTG ACT TAC CTG CAT CAC CAT GGT CAT GAA GAT AAG	864
Trp Leu Asp Phe Val Thr Tyr Leu His His His Gly His Glu Asp Lys	
275 280 285	
CTC CCT TGG TAC CGT GGG AAG GAA TGG AGT TAC TTG AGA GGA GGA CTT	912
Leu Pro Trp Tyr Arg Gly Lys Glu Trp Ser Tyr Leu Arg Gly Gly Leu	
290 295 300	
ACA ACA TTG GAC CGG GAC TAC GGA TTG ATC AAC AAC ATC CAT CAC GAC	960
Thr Thr Leu Asp Arg Asp Tyr Gly Leu Ile Asn Asn Ile His His Asp	
305 310 315 320	
ATT GGA ACT CAT GTG ATA CAT CAT CTT TTC CCT CAG ATC CCA CAT TAT	1008
Ile Gly Thr His Val Ile His His Leu Phe Pro Gln Ile Pro His Tyr	
325 330 335	
CAT CTA GTA GAA GCA ACA GAA GCA GCT AAA CCA GTA TTA GGG AAG TAT	1056
His Leu Val Glu Ala Thr Glu Ala Ala Lys Pro Val Leu Gly Lys Tyr	
340 345 350	
TAT AGG GAG CCT GAT AAG TCT GGA CCT TTG CCA TTA CAT TTA CTG GGA	1104
Tyr Arg Glu Pro Asp Lys Ser Gly Pro Leu Pro Leu His Leu Leu Gly	
355 360 365	
ATC TTA GCA AAA AGT ATT AAA GAA GAT CAT TTT GTG AGC GAT GAA GGA	1152
Ile Leu Ala Lys Ser Ile Lys Glu Asp His Phe Val Ser Asp Glu Gly	
370 375 380	
GAT GTT GTA TAC TAT GAA GCA GAC CCT AAT CTC TAT GGA GAG ATC AAG	1200
Asp Val Val Tyr Tyr Glu Ala Asp Pro Asn Leu Tyr Gly Glu Ile Lys	
385 390 395 400	
GTA ACA GCA GAG TGAAATGAAG CTGTCAGATT TATCTATTTT TGACCAGCTG	1252
Val Thr Ala Glu	
405	
ATTTTTTTTG CTTATTAATG TCAATTCATT GTGTTACCAT TATCTCTGAA TACAATCAGA	1312
TGGAAACCCC AACTTTGTTT TCAATACTTG AAGCTATATA TATATATATA TATGTAAGAT	1372
ACATTGTATT GTCATTAGAT TCACCATTCT CAAGGTTCTT ATACAAAAAA AAAAAA	1429

SECRET "SECRET"

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Phe 1	Lys	Phe	Arg	Gln 5	Ser	Pro	Ser	Ser	Pro 10	Arg	Phe	Arg	Leu	Asn 15	Ser
Arg	Asn	Trp	Ala 20	Leu	Asn	Val	Thr	Thr 25	Pro	Leu	Thr	Val	Asp 30	Ser	Ser
Ser	Ser	Pro 35	Pro	Ile	Glu	Glu	Glu 40	Pro	Lys	Thr	Gln	Arg 45	Phe	Asp	Pro
Gly	Ala 50	Pro	Pro	Pro	Phe	Asn 55	Leu	Ala	Asp	Ile	Arg 60	Ala	Ala	Ile	Pro
Lys 65	His	Cys	Trp	Val	Lys 70	Asn	Pro	Trp	Lys	Ser 75	Met	Ser	Tyr	Val	Val 80
Arg	Glu	Leu	Ala	Ile 85	Val	Phe	Ala	Leu	Ala 90	Ala	Gly	Ala	Ala	Tyr 95	Leu
Asn	Asn	Trp	Leu 100	Val	Trp	Pro	Leu	Tyr 105	Trp	Ile	Ala	Gln	Gly 110	Thr	Met
Phe	Trp	Ala 115	Leu	Phe	Val	Leu	Gly 120	His	Asp	Cys	Gly	His 125	Gly	Ser	Phe
Ser	Asn	Asp	Pro	Arg	Leu	Asn 135	Ser	Val	Val	Gly	His 140	Leu	Leu	His	Ser
Ser 145	Ile	Leu	Val	Pro	Tyr 150	His	Gly	Trp	Arg	Ile 155	Ser	His	Arg	Thr	His 160
His	Gln	Asn	His	Gly 165	His	Val	Glu	Asn	Asp 170	Glu	Ser	Trp	His	Pro 175	Met
Ser	Glu	Lys	Ile 180	Tyr	Lys	Ser	Leu	Asp 185	Lys	Pro	Thr	Arg	Phe 190	Phe	Arg
Phe	Thr	Leu 195	Pro	Leu	Val	Met	Leu 200	Ala	Tyr	Pro	Phe	Tyr 205	Leu	Trp	Ala
Arg	Ser 210	Pro	Gly	Lys	Lys	Gly 215	Ser	His	Tyr	His	Pro 220	Asp	Ser	Asp	Leu
Phe 225	Leu	Pro	Lys	Glu	Arg 230	Asn	Asp	Val	Leu	Thr 235	Ser	Thr	Ala	Cys	Trp 240

Thr Ala Met Ala Val Leu Leu Val Cys Leu Asn Phe Val Met Gly Pro
 245 250 255
 Met Gln Met Leu Lys Leu Tyr Val Ile Pro Tyr Trp Ile Asn Val Met
 260 265 270
 Trp Leu Asp Phe Val Thr Tyr Leu His His His Gly His Glu Asp Lys
 275 280 285
 Leu Pro Trp Tyr Arg Gly Lys Glu Trp Ser Tyr Leu Arg Gly Gly Leu
 290 295 300
 Thr Thr Leu Asp Arg Asp Tyr Gly Leu Ile Asn Asn Ile His His Asp
 305 310 315 320
 Ile Gly Thr His Val Ile His His Leu Phe Pro Gln Ile Pro His Tyr
 325 330 335
 His Leu Val Glu Ala Thr Glu Ala Ala Lys Pro Val Leu Gly Lys Tyr
 340 345 350
 Tyr Arg Glu Pro Asp Lys Ser Gly Pro Leu Pro Leu His Leu Leu Gly
 355 360 365
 Ile Leu Ala Lys Ser Ile Lys Glu Asp His Phe Val Ser Asp Glu Gly
 370 375 380
 Asp Val Val Tyr Tyr Glu Ala Asp Pro Asn Leu Tyr Gly Glu Ile Lys
 385 390 395 400
 Val Thr Ala Glu

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Glycine max

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pXF1

(ix) FEATURE:

- (A) NAME/KEY: CDS

SECRET - 5661258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACAATAATAA ATCCATATTT TTATAATTAA AAGTAGTAGA TTACAGCGAT GCACTTGAGA	60
AACATATTAA GTGGACTAAT TCTCCCTGGT CAAGCAAGAA AAAAACCAGC TATGACCCAA	120
GGTAGAGAGA GATTATACAC AGAATACTAG TAATTAAC TAAGACTGGCTC TGCAATTGCC	180
AAAACTCCA TTGCAGTAGC AGCCACCTGA GAAGACACTA AGACCTAGAC TAGACCATAC	240
ATATGAAGAT TAATACGCTT ACATAACAAC ATAGGACACT AAGAAAACAC GGCTTACAGA	300
GAATCCAGCT GACTCTATAA GAGGGGTACT TCTGGAGATT AAAATTATCC GAATCACCTT	360
CCCACTGCGG CTGCTGACGT CAGCGAAAGT CAGAACCGAA AGCGGCGAAG AACCTTCAGA	420
AGAGGAGGAA GCACTTCGAC CTTACAAGAG TTGTTGTCGT TGTGTTGTC GTTCTCTGGC	480
GGAGAAGCGA GTTTGGATCG CGTTTTCTC GGAGGCTTCT CGGTCTTCCC CTGTTTCTGC	540
AGCTCAGCCA GGCCCTCGCA AATGGCCTGA AGCTTGCGCT CAACGGCGGA ATGAAGAGGC	600
TAATACTCCC CGAAGTCACC ACCGACGGAG GAACCCTGGT GTCGGAGGTT GGGGAAGTTG	660
AGCCTGGCGA AGTCACCTCG GAGCTTGAC GCGGCCTTGT GGTACGCCAG AGCGGCTTCC	720
TCGGCGGTGT CGAAGGTTCC CAGCCATAGC CTGGTCCGGA TTCTTCGGGA GTCTAATCTC	780
AGCCACCCAC TTCCCCCTG AGAAAAGAGA GGAACCACAC TCTCTAAGCC AAAGCAAAAG	840
CAGCAGCAGC AGCA ATG GTT AAA GAC ACA AAG CCT TTA GCC TAT GCT GCC	890
Met Val Lys Asp Thr Lys Pro Leu Ala Tyr Ala Ala	
1 5 10	
AAT AAT GGA TAC CAA CAA AAG GGT TCT TCT TTT GAT TTT GAT CCT AGC	938
Asn Asn Gly Tyr Gln Gln Lys Gly Ser Ser Phe Asp Phe Asp Pro Ser	
15 20 25	
GCT CCT CCA CCG TTT AAG ATT GCA GAA ATC AGA GCT TCA ATA CCA AAA	986
Ala Pro Pro Pro Phe Lys Ile Ala Glu Ile Arg Ala Ser Ile Pro Lys	
30 35 40	
CAT TGC TGG GTC AAG AAT CCA TGG AGA TCC CTC AGT TAT GTT CTC AGG	1034
His Cys Trp Val Lys Asn Pro Trp Arg Ser Leu Ser Tyr Val Leu Arg	
45 50 55 60	
GAT GTG CTT GTA ATT GCT GCA TTG GTG GCT GCA GCA ATT CAC TTC GAC	1082
Asp Val Leu Val Ile Ala Ala Leu Val Ala Ala Ala Ile His Phe Asp	
65 70 75	
AAC TGG CTT CTC TGG CTA ATC TAT TGC CCC ATT CAA GGC ACA ATG TTC	1130
Asn Trp Leu Leu Trp Leu Ile Tyr Cys Pro Ile Gln Gly Thr Met Phe	
80 85 90	

TGG	GCT	CTC	TTT	GTT	CTT	GGA	CAT	GAT	TGT	GGC	CAT	GGA	AGC	TTT	TCA	1178
Trp	Ala	Leu	Phe	Val	Leu	Gly	His	Asp	Cys	Gly	His	Gly	Ser	Phe	Ser	
	95						100					105				
GAT	AGC	CCT	TTG	CTG	AAT	AGC	CTG	GTG	GGA	CAC	ATC	TTG	CAT	TCC	TCA	1226
Asp	Ser	Pro	Leu	Leu	Asn	Ser	Leu	Val	Gly	His	Ile	Leu	His	Ser	Ser	
	110					115					120					
ATT	CTT	GTG	CCA	TAC	CAT	GGA	TGG	AGA	ATT	AGC	CAC	AGA	ACT	CAC	CAT	1274
Ile	Leu	Val	Pro	Tyr	His	Gly	Trp	Arg	Ile	Ser	His	Arg	Thr	His	His	
125					130					135					140	
CAA	AAC	CAT	GGA	CAC	ATT	GAG	AAG	GAT	GAG	TCA	TGG	GTT	CCA	TTA	ACA	1322
Gln	Asn	His	Gly	His	Ile	Glu	Lys	Asp	Glu	Ser	Trp	Val	Pro	Leu	Thr	
			145						150					155		
GAG	AAG	ATT	TAC	AAG	AAT	CTA	GAC	AGC	ATG	ACA	AGA	CTC	ATT	AGA	TTC	1370
Glu	Lys	Ile	Tyr	Lys	Asn	Leu	Asp	Ser	Met	Thr	Arg	Leu	Ile	Arg	Phe	
			160					165					170			
ACT	GTG	CCA	TTT	CCA	TTG	TTT	GTG	TAT	CCA	ATT	TAT	TTG	TTT	TCA	AGA	1418
Thr	Val	Pro	Phe	Pro	Leu	Phe	Val	Tyr	Pro	Ile	Tyr	Leu	Phe	Ser	Arg	
	175						180					185				
AGC	CCC	GGA	AAG	GAA	GGC	TCT	CAC	TTC	AAT	CCC	TAC	AGC	AAT	CTG	TTC	1466
Ser	Pro	Gly	Lys	Glu	Gly	Ser	His	Phe	Asn	Pro	Tyr	Ser	Asn	Leu	Phe	
	190					195					200					
CCA	CCC	AGT	GAG	AGA	AAA	GGA	ATA	GCA	ATA	TCA	ACA	CTG	TGT	TGG	GCT	1514
Pro	Pro	Ser	Glu	Arg	Lys	Gly	Ile	Ala	Ile	Ser	Thr	Leu	Cys	Trp	Ala	
205					210					215					220	
ACC	ATG	TTT	TCT	CTG	CTT	ATC	TAT	CTC	TCA	TTC	ATA	ACT	AGT	CCA	CTT	1562
Thr	Met	Phe	Ser	Leu	Leu	Ile	Tyr	Leu	Ser	Phe	Ile	Thr	Ser	Pro	Leu	
				225					230					235		
CTA	GTG	CTC	AAG	CTC	TAT	GGA	ATT	CCA	TAT	TGG	ATA	TTT	GTT	ATG	TGG	1610
Leu	Val	Leu	Lys	Leu	Tyr	Gly	Ile	Pro	Tyr	Trp	Ile	Phe	Val	Met	Trp	
			240					245					250			
CTG	GAC	TTT	GTC	ACA	TAC	TTG	CAT	CAC	CAT	GGT	CAC	CAC	CAG	AAA	CTG	1658
Leu	Asp	Phe	Val	Thr	Tyr	Leu	His	His	His	Gly	His	His	Gln	Lys	Leu	
	255						260					265				
CCT	TGG	TAC	CGC	GGC	AAG	GAA	TGG	AGT	TAT	TTA	AGA	GGT	GGC	CTC	ACC	1706
Pro	Trp	Tyr	Arg	Gly	Lys	Glu	Trp	Ser	Tyr	Leu	Arg	Gly	Gly	Leu	Thr	
	270					275					280					
ACT	GTG	GAT	CGT	GAC	TAT	GGT	TGG	ATC	TAT	AAC	ATT	CAC	CAT	GAC	ATT	1754
Thr	Val	Asp	Arg	Asp	Tyr	Gly	Trp	Ile	Tyr	Asn	Ile	His	His	Asp	Ile	
285					290					295					300	
GGC	ACC	CAT</														

(2) INFORMATION FOR SEQ ID NO:11:

(A) LENGTH: 380 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Val	Lys	Asp	Thr	Lys	Pro	Leu	Ala	Tyr	Ala	Ala	Asn	Asn	Gly	Tyr
1				5					10					15	
Gln	Gln	Lys	Gly	Ser	Ser	Phe	Asp	Phe	Asp	Pro	Ser	Ala	Pro	Pro	Pro
			20					25					30		
Phe	Lys	Ile	Ala	Glu	Ile	Arg	Ala	Ser	Ile	Pro	Lys	His	Cys	Trp	Val
		35					40					45			
Lys	Asn	Pro	Trp	Arg	Ser	Leu	Ser	Tyr	Val	Leu	Arg	Asp	Val	Leu	Val
	50					55					60				
Ile	Ala	Ala	Leu	Val	Ala	Ala	Ala	Ile	His	Phe	Asp	Asn	Trp	Leu	Leu
65					70					75					80
Trp	Leu	Ile	Tyr	Cys	Pro	Ile	Gln	Gly	Thr	Met	Phe	Trp	Ala	Leu	Phe
				85					90					95	
Val	Leu	Gly	His	Asp	Cys	Gly	His	Gly	Ser	Phe	Ser	Asp	Ser	Pro	Leu
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:12:

(A) LENGTH: 1675 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Glycine max

(vii) IMMEDIATE SOURCE:

(B) CLONE: pSFD-118bwp

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 169..1530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTGTGGCAAT TTTTCTCTTC TCCTTCTGGT TCTCATCTTT GTGTTCTTCT TTGTTTCTCA	60
CCTTTCTGAG GATTTTTCCTA TCTTAGTTCC TGGAGGCACC AGGAACCTGA CCAAATAAAT	120
AAACCTTTTT TTTCTTCTAA TTTTCTGAA GTTTCATTTT TTAGTCCA ATG GCA ACT	177
Met Ala Thr	
1	
TGG TAT CAT CAG AAA TGT GGC TTG AAG CCT CTT GCT CCA GTA ATT CCT	225
Trp Tyr His Gln Lys Cys Gly Leu Lys Pro Leu Ala Pro Val Ile Pro	
5 10 15	
AGA CCT AGA ACT GGG GCT GCT TTG TCC AGC ACC TCA AGG GTT GAA TTT	273
Arg Pro Arg Thr Gly Ala Ala Leu Ser Ser Thr Ser Arg Val Glu Phe	
20 25 30 35	
TTG GAC ACA AAC AAG GTA GTG GCA GGT CCT AAG TTT CAA CCT TTG AGG	321
Leu Asp Thr Asn Lys Val Val Ala Gly Pro Lys Phe Gln Pro Leu Arg	
40 45 50	
TGC AAC CTC AGG GAG AGG AAT TGG GGG CTG AAA GTG AGT GCC CCT TTG	369
Cys Asn Leu Arg Glu Arg Asn Trp Gly Leu Lys Val Ser Ala Pro Leu	
55 60 65	
AGG GTT GCT TCC ATT GAA GAG GAG CAA AAG AGT GTT GAT TTA ACC AAT	417
Arg Val Ala Ser Ile Glu Glu Glu Gln Lys Ser Val Asp Leu Thr Asn	
70 75 80	
GGG ACT AAT GGG GTT GAG CAT GAG AAG CTT CCA GAA TTT GAC CCT GGT	465
Gly Thr Asn Gly Val Glu His Glu Lys Leu Pro Glu Phe Asp Pro Gly	
85 90 95	
GCT CCG CCA CCA TTC AAC TTG GCT GAT ATT AGA GCA GCC ATT CCA AAG	513
Ala Pro Pro Pro Phe Asn Leu Ala Asp Ile Arg Ala Ala Ile Pro Lys	
100 105 110 115	

05219935 122393

CAT His	TGC Cys	TGG Trp	GTG Val	AAG Lys 120	GAC Asp	CCT Pro	TGG Trp	AGG Arg	TCC Ser 125	ATG Met	AGC Ser	TAT Tyr	GTG Val	GTG Val 130	AGG Arg	561
GAT Asp	GTG Val	ATT Ile	GCT Ala 135	GTC Val	TTT Phe	GGT Gly	TTG Leu	GCT Ala 140	GCT Ala	GCT Ala	GCT Ala	GCG Ala 145	TAT Tyr	CTC Leu	AAT Asn	609
AAT Asn	TGG Trp	TTG Leu 150	GTT Val	TGG Trp	CCT Pro	CTC Leu	TAT Tyr 155	TGG Trp	GCT Ala	GCT Ala	CAA Gln	GGC Gly 160	ACT Thr	ATG Met	TTC Phe	657
TGG Trp	GCT Ala 165	CTG Leu	TTT Phe	GTT Val	CTT Leu	GGT Gly 170	CAT His	GAT Asp	TGT Cys	GGT Gly	CAT His 175	GGA Gly	AGC Ser	TTT Phe	TCA Ser	705
AAC Asn 180	AAC Asn	TCC Ser	AAA Lys	TTG Leu	AAC Asn 185	AGT Ser	GTT Val	GTT Val	GGA Gly	CAT His 190	CTG Leu	CTG Leu	CAT His	TCT Ser	TCA Ser 195	753
ATT Ile	CTA Leu	GTG Val	CCA Pro 200	TAT Tyr	CAT His	GGA Gly	TGG Trp	AGA Arg 205	ATC Ile	AGT Ser	CAT His	AGG Arg	ACT Thr	CAT His 210	CAC His	801
CAA Gln	CAT His	CAT His	GGT Gly 215	CAT His	GCT Ala	GAA Glu	AAT Asn 220	GAT Asp	GAA Glu	TCA Ser	TGG Trp	CAT His 225	CCG Pro	TTG Leu	CCT Pro	849
GAA Glu	AAA Lys 230	TTG Leu	TTC Phe	AGA Arg	AGC Ser	TTG Leu	GAC Asp 235	ACT Thr	GTA Val	ACT Thr	CGT Arg	ATG Met 240	TTA Leu	AGA Arg	TTC Phe	897
ACA Thr	GCA Ala 245	CCT Pro	TTT Phe	CCA Pro	CTT Leu	CTT Leu 250	GCA Ala	TTT Phe	CCT Pro	GTG Val	TAC Tyr 255	CTT Leu	TTT Phe	AGT Ser	AGG Arg	945
AGT Ser 260	CCT Pro	GGG Gly	AAG Lys	ACT Thr	GGT Gly 265	TCT Ser	CAC His	TTT Phe	GAC Asp 270	CCC Pro	AGC Ser	AGT Ser	GAC Asp	TTG Leu	TTC Phe 275	993
GTT Val	CCC Pro	AAT Asn	GAA Glu	AGA Arg 280	AAA Lys	GAT Asp	GTT Val	ATT Ile	ACT Thr 285	TCC Ser	ACA Thr	GCT Ala	TGT Cys	TGG Trp 290	GCT Ala	1041
GCT Ala	ATG Met	TTG Leu	GGA Gly 295	TTG Leu	CTT Leu	GTT Val	GGA Gly	TTG Leu 300	GGG Gly	TTT Phe	GTA Val	ATG Met	GGT Gly 305	CCA Pro	ATT Ile	1089
CAA Gln	CTT Leu	CTT Leu 310	AAG Lys	CTT Leu	TAT Tyr	GGT Gly	GTT Val 315	CCC Pro	TAT Tyr	GTT Val	ATA Ile	TTC Phe 320	GTT Val	ATG Met	TGG Trp	1137
TTG Leu	GAT Asp 325	TTG Leu	GTG Val	ACT Thr	TAT Tyr 330	TTG Leu	CAC His	CAT His	CAT His	GGC Gly 335	CAT His	GAA Glu	GAC Asp	AAA Lys	TTA Leu	1185

(2) INFORMATION FOR SEQ ID NO:13:

(A) LENGTH: 453 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ala	Thr	Trp	Tyr	His	Gln	Lys	Cys	Gly	Leu	Lys	Pro	Leu	Ala	Pro
1				5					10					15	
Val	Ile	Pro	Arg	Pro	Arg	Thr	Gly	Ala	Ala	Leu	Ser	Ser	Thr	Ser	Arg
			20					25					30		
Val	Glu	Phe	Leu	Asp	Thr	Asn	Lys	Val	Val	Ala	Gly	Pro	Lys	Phe	Gln
		35					40					45			

Pro 50	Leu	Arg	Cys	Asn	Leu	Arg	Glu	Arg	Asn	Trp	Gly	Leu	Lys	Val	Ser
Ala 65	Pro	Leu	Arg	Val	Ala 70	Ser	Ile	Glu	Glu	Glu	Gln	Lys	Ser	Val	Asp 80
Leu	Thr	Asn	Gly	Thr 85	Asn	Gly	Val	Glu	His 90	Glu	Lys	Leu	Pro	Glu	Phe 95
Asp	Pro	Gly	Ala 100	Pro	Pro	Pro	Phe	Asn 105	Leu	Ala	Asp	Ile	Arg 110	Ala	Ala
Ile	Pro	Lys 115	His	Cys	Trp	Val	Lys 120	Asp	Pro	Trp	Arg 125	Ser	Met	Ser	Tyr
Val	Val 130	Arg	Asp	Val	Ile	Ala 135	Val	Phe	Gly	Leu	Ala 140	Ala	Ala	Ala	Ala
Tyr 145	Leu	Asn	Asn	Trp	Leu 150	Val	Trp	Pro	Leu	Tyr 155	Trp	Ala	Ala	Gln	Gly 160
Thr	Met	Phe	Trp	Ala 165	Leu	Phe	Val	Leu	Gly 170	His	Asp	Cys	Gly	His 175	Gly
Ser	Phe	Ser	Asn 180	Asn	Ser	Lys	Leu	Asn 185	Ser	Val	Val	Gly	His 190	Leu	Leu
His	Ser	Ser 195	Ile	Leu	Val	Pro	Tyr 200	His	Gly	Trp	Arg 205	Ile	Ser	His	Arg
Thr	His 210	His	Gln	His	His	Gly 215	His	Ala	Glu	Asn	Asp 220	Glu	Ser	Trp	His
Pro 225	Leu	Pro	Glu	Lys	Leu 230	Phe	Arg	Ser	Leu	Asp 235	Thr	Val	Thr	Arg	Met 240
Leu	Arg	Phe	Thr	Ala 245	Pro	Phe	Pro	Leu	Leu	Ala	Phe	Pro	Val	Tyr 255	Leu
Phe	Ser	Arg	Ser 260	Pro	Gly	Lys	Thr	Gly 265	Ser	His	Phe	Asp	Pro 270	Ser	Ser
Asp	Leu	Phe 275	Val	Pro	Asn	Glu	Arg 280	Lys	Asp	Val	Ile	Thr 285	Ser	Thr	Ala
Cys	Trp 290	Ala	Ala	Met	Leu	Gly 295	Leu	Leu	Val	Gly	Leu 300	Gly	Phe	Val	Met
Gly 305	Pro	Ile	Gln	Leu	Leu 310	Lys	Leu	Tyr	Gly	Val 315	Pro	Tyr	Val	Ile	Phe 320
Val	Met	Trp	Leu	Asp 325	Leu	Val	Thr	Tyr	Leu 330	His	His	His	Gly	His 335	Glu
Asp	Lys	Leu	Pro	Trp	Tyr	Arg	Gly	Lys 345	Glu	Trp	Ser	Tyr	Leu 350	Arg	Gly

Gly Leu Thr Thr Leu Asp Arg Asp Tyr Gly Trp Ile Asn Asn Ile His
 355 360 365
 His Asp Ile Gly Thr His Val Ile His His Leu Phe Pro Gln Ile Pro
 370 375 380
 His Tyr His Leu Val Glu Ala Thr Glu Ala Ala Lys Pro Val Phe Gly
 385 390 395 400
 Lys Tyr Tyr Arg Glu Pro Lys Lys Ser Ala Ala Pro Leu Pro Phe His
 405 410 415
 Leu Ile Gly Glu Ile Ile Arg Ser Phe Lys Thr Asp His Phe Val Ser
 420 425 430
 Asp Thr Gly Asp Val Val Tyr Tyr Gln Thr Asp Ser Lys Ile Asn Gly
 435 440 445
 Ser Ser Lys Leu Glu
 450

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pPCR20

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 31..363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGATCCACGC ATCATCAGAA TCACGGTCAC ATCCACAGGG ACGAGTCATG GCACCCGATC	60
ACGGAGAAGC TGTACCGGCA ACTAGAGCCA CGCACCAAGA AGCTGAGATT CACGGTGCCC	120
TTCCCCCTGC TCGCATTCCC CGTCTACCTC TTGTACAGGA GCCCCGGCAA GCTCGGCTCC	180
CACTTCCTTC CCAGCAGCGA CCTGTTCAGC CCCAAGGAGA AGAGCGACGT CATGGTGTCA	240

ACCACCTGCT GGTGCATCAT GCTCGCCTCC CTCCTCGCCA TGGCGTGCGC GTTCGGCCCA 300
 CTCCAGGTGC TCAAGATGTA CGGCATCCCA TACCTGGTGT TCGTGATGTG GCTTGACCTG 360
 GTGACGTACT TACATCACCA CGGCCACGAT GGATCC 396

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(vii) IMMEDIATE SOURCE:

(B) CLONE: pPCR20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His	His	Gln	Asn	His	Gly	His	Ile	His	Arg	Asp	Glu	Ser	Trp	His	Pro	1	5	10	15
Ile	Thr	Glu	Lys	Leu	Tyr	Arg	Gln	Leu	Glu	Pro	Arg	Thr	Lys	Lys	Leu	20	25	30	
Arg	Phe	Thr	Val	Pro	Phe	Pro	Leu	Leu	Ala	Phe	Pro	Val	Tyr	Leu	Leu	35	40	45	
Tyr	Arg	Ser	Pro	Gly	Lys	Leu	Gly	Ser	His	Phe	Leu	Pro	Ser	Ser	Asp	50	55	60	
Leu	Phe	Ser	Pro	Lys	Glu	Lys	Ser	Asp	Val	Met	Val	Ser	Thr	Thr	Cys	65	70	75	80
Trp	Cys	Ile	Met	Leu	Ala	Ser	Leu	Leu	Ala	Met	Ala	Cys	Ala	Phe	Gly	85	90	95	
Pro	Leu	Gln	Val	Leu	Lys	Met	Tyr	Gly	Ile	Pro	Tyr	Leu	Val	Phe	Val	100	105	110	
Met	Trp	Leu	Asp	Leu	Val	Thr	Tyr	Leu	His	His	His	Gly	His			115	120	125	

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(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: pFadx-2 and pYacp7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCGAGCTA	CGTCAGGGCT	AAAACCAGGA	ACTGGGCATT	GAATGTGGCA	ACACCTTTAA	60
CAACTCTTCA	GTCCTCCATCC	GAGGAAGACA	GGGAGAGATT	CGACCCAGGT	GCGCCTCCTC	120
CCTTCAATTT	GGCGGATATA	AGAGCAGCCA	TACCTAAGCA	TTGTTGGGTT	AAGAATCCAT	180
GGATGTCTAT	GAGTTATGTT	GTCAGAGATG	TTGCTATCGT	CTTTGGATTG	GCTGCTGTTG	240
CTGCTTACTT	CAACAATTGG	CTTCTCTGGC	CTCTCTACTG	GTTCGCTCAA	GGAACCATGT	300
TCTGGGCTCT	CTTTGTCCTT	GGCCATGACT	GCGGACATGG	TAGCTTCTCG	AATGATCCGA	360
GGCTGAACAG	TGTGGCTGGT	CATCTTCTTC	ATTCCTCAAT	CCTGGTCCCT	TACCATGGCT	420
GGAGGATTAG	CCACAGAACT	CACCACCAGA	ACCATGGTCA	TGTCGAGAAT	GA	472

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii). MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) CLONE: pFadx-2 and pYacp7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ser 1	Ser	Tyr	Val	Arg 5	Ala	Lys	Thr	Arg	Asn 10	Trp	Ala	Leu	Asn	Val 15	Ala
Thr	Pro	Leu	Thr 20	Thr	Leu	Gln	Ser	Pro 25	Ser	Glu	Glu	Asp	Arg 30	Glu	Arg
Phe	Asp	Pro 35	Gly	Ala	Pro	Pro	Pro 40	Phe	Asn	Leu	Ala	Asp 45	Ile	Arg	Ala
Ala	Ile 50	Pro	Lys	His	Cys	Trp 55	Val	Lys	Asn	Pro	Trp 60	Met	Ser	Met	Ser
Tyr 65	Val	Val	Arg	Asp 70	Val	Ala	Ile	Val	Phe	Gly 75	Leu	Ala	Ala	Val	Ala 80
Ala	Tyr	Phe	Asn 85	Asn	Trp	Leu	Leu	Trp 90	Pro	Leu	Tyr	Trp	Phe	Ala 95	Gln
Gly	Thr	Met	Phe 100	Trp	Ala	Leu	Phe	Val 105	Leu	Gly	His	Asp	Cys 110	Gly	His
Gly	Ser	Phe 115	Ser	Asn	Asp	Pro	Arg 120	Leu	Asn	Ser	Val	Ala 125	Gly	His	Leu
Leu	His 130	Ser	Ser	Ile	Leu	Val 135	Pro	Tyr	His	Gly	Trp 140	Arg	Ile	Ser	His
Arg 145	Thr	His	His	Gln	Asn 150	His	Gly	His	Val	Glu	Asn 155				

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) **FEATURE:**

- (A) NAME/KEY: misc feature
(B) LOCATION: 1..11
(D) OTHER INFORMATION: /note= "N= INOSINE"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION: 12..31
(D) OTHER INFORMATION: /note= "N= A OR T OR G OR C"

31

35

CGGGATCCRT CRTGNCCRTG RTGRTGNARR TANGT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

42

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "N= INOSINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTCGTNNTNG GNCAYGAYTG YGGNCAYGGN TCNTTC

36

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGHCAYGAYT GYGGHAC

18

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGHCAYGAYT GYGGHACAT

18

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTACTRTARC CDTGDGTR

18

855227 5557260

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTGCTRTARC CDTGDGTR

18

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTRCANTARG TRGTRAAYAA YGG

23

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTRCANTADG TRGTRGADAA YGG

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "N= INOSINE"

0020995 12393 866221 5666250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTCGTNNTNG GNCAYGAYTG YGGNCAYGGN AGNTTT

36

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "N= INOSINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTCGTNNTNG GNCAYGAYTG YGGNCAYGGN TCNTTT

36

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: /note= "N= INOSINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTRCTRTANC CNTGNGTNCA NTANGTAGTG RANAAGGG

38

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..38

(D) OTHER INFORMATION: /note= "N= INOSINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTRCTRTANC CNTGNGTNCA NTANGTGGTG RANAAGGG

38

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: /note= "N= INOSINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GTGGTGNGTN CNGTGNGANA NNCKCCANCC GTGGTANGGN ACNANNANGA ANGANGAGTG

60

NANNANGTGN CCNACNANNG AGTTNANNAN NGGNATNTCN GAGAANGANC CGTGNCCGCA

120

NTCGTGNCN ANNACGAA

138

SECRET - 50501250